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RAW SEQUENCE LISTING

DATE: 06/03/2002

PATENT APPLICATION: US/10/014,320

TIME: 12:50:36

Input Set : A:\EP.txt

Output Set: N:\CRF3\06032002\J014320.raw

IN

3 <110> APPLICANT: North Shore - Long Island Jewish Research Institute
 4 Tabibzadeh, Siamak
 6 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING A PRE-NEOPLASTIC OR NEOPLASTIC LESION

7 TRANSITIONAL EPITHELIAL CELLS
 9 <130> FILE REFERENCE: 50425/137
 11 <140> CURRENT APPLICATION NUMBER: 10/014,320
 12 <141> CURRENT FILING DATE: 2001-12-11
 14 <150> PRIOR APPLICATION NUMBER: 60/255,641
 15 <151> PRIOR FILING DATE: 2000-12-14
 17 <160> NUMBER OF SEQ ID NOS: 6
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1161
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <400> SEQUENCE: 1

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29	tggctctgct	gggcaactctg	ggtgtctgcc	ctggttgcc	ccggggcggc	cctgaccgag	120
31	gagcagctcc	tgggcagcct	gctgcggcag	ctgcagctca	gcgaggtgcc	cgtactggac	180
33	agggccgaca	tggagaagct	ggtcatcccc	gcccacgtga	gggcccagta	tgtagtccctg	240
35	ctgcggcgca	gccacgggga	ccgctccccg	ggaaagaggt	tcagccagag	cttccgagag	300
37	gtggccggca	ggttccttgc	gtcggaggcc	agcacacacc	tgctggtgtt	cggcattggag	360
39	cagcggctgc	cgcccaacag	cgagctggtg	caggccgtgc	tgcggctctt	ccaggagccg	420
41	gtccccaagg	ccgcgctgca	caggcacggg	cggctgtccc	cgcgacgcgc	ccaggcccgg	480
43	gtgaccgtcg	agtggctgcg	cgtccgcgac	gacggctcca	accgcacctc	cctcatcgac	540
45	tccaggtcgg	tgtccgtcca	cgagagcggc	tggaaaggcct	tcgacgtgac	cgaggccgtg	600
47	aacttctggc	agcagctgag	ccggccccgg	cagccgctgc	tgtacaggt	gtcgggtgcag	660
49	agggagcatc	tgggcccgt	ggcgtccggc	gcccacaagc	tggtcogctt	tgctcgcag	720
51	ggggcgccag	ccgggcttgg	ggagccccag	ctggagctgc	acaccctgga	cctcagggac	780
53	tatggagctc	agggcgactg	tgaccctgaa	gcaccaatga	ccgagggcac	ccgctgctgc	840
55	cgccaggaga	tgtacattga	cctgcagggg	atgaagtggg	ccaagaactg	ggtgctggag	900
57	cccccgggct	tcctggctta	cgagtgtgtg	ggcacctgcc	agcagcccc	ggaggccctg	960
59	gccttcaatt	ggccatttct	ggggcccgca	cagtgtatcg	cctcggagac	tgctcgcgtg	1020
61	cccatgatcg	tcagcatcaa	ggagggaggc	aggaccaggc	cccaggtggt	cagcctgccc	1080
63	aacatgaggg	tgcagaagtg	cagctgtgcc	tcggatgggg	cgctcgtgcc	aaggaggctc	1140
65	cagccatagg	cgctgtgtgt	a				1161

68 <210> SEQ ID NO: 2
 69 <211> LENGTH: 366
 70 <212> TYPE: PRT
 71 <213> ORGANISM: Homo sapiens
 73 <400> SEQUENCE: 2
 75 Met Trp Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 76 1 5 10 15

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79 Gly Pro Gly Ala Ala Leu Thr Glu Glu Gln Leu Leu Gly Ser Leu Leu
80          20          25          30
83 Arg Gln Leu Gln Leu Ser Glu Val Pro Val Leu Asp Arg Ala Asp Met
84          35          40          45
87 Glu Lys Leu Val Ile Pro Ala His Val Arg Ala Gln Tyr Val Val Leu
88          50          55          60
91 Leu Arg Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
92 65          70          75          80
95 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Ser Glu Ala Ser Thr
96          85          90          95
99 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
100          100          105          110
103 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
104          115          120          125
107 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Gln Ala Arg
108          130          135          140
111 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
112 145          150          155          160
115 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
116          165          170          175
119 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
120          180          185          190
123 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
124          195          200          205
127 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
128          210          215          220
131 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
132 225          230          235          240
135 Asp Leu Arg Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
136          245          250          255
139 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
140          260          265          270
143 Gln Gly Met Lys Trp Ala Lys Asn Trp Val Leu Glu Pro Pro Gly Phe
144          275          280          285
147 Leu Ala Tyr Glu Cys Val Gly Thr Cys Gln Gln Pro Pro Glu Ala Leu
148          290          295          300
151 Ala Phe Asn Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
152 305          310          315          320
155 Thr Ala Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
156          325          330          335
159 Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
160          340          345          350
163 Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
164          355          360          365
167 <210> SEQ ID NO: 3
168 <211> LENGTH: 36
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:

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173 <223> OTHER INFORMATION: forward primer
175 <400> SEQUENCE: 3
176 agaattcaag atgtggcccc tgtggctctg ctgggc 36
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 40
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: reverse primer
187 <400> SEQUENCE: 4
188 ttctagacta tggctggagc ctccttggca cgagcgcccc 40
191 <210> SEQ ID NO: 5
192 <211> LENGTH: 44
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: forward primer
199 <400> SEQUENCE: 5
200 gcgtccgcga cgacggctcc gaccgcacct ccctcatcga ctcc 44
203 <210> SEQ ID NO: 6
204 <211> LENGTH: 44
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: reverse primer
211 <400> SEQUENCE: 6
212 ggagtcgatg agggaggtgc ggtcggagcc gtcgtcgcgg acgc 44

VERIFICATION SUMMARY

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